



MEDLINE PUBLMED REFERENCE AUTHORS	20330913 1107681 4 (sites) The RIKEN Genome Exploration Research Group Phase II Team and the FAIRY Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5 (bases 1 to 2696)
AUTHORS	Adachi,J., Aizawa,R., Akahira,S., Akimura,T., Aono,H., Arai,A., Arikawa,T., Baldarelli,R., Bonio,H., Brownstein,M., Built,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hirooka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,I., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shiba,T., Shinzawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamakawa,I., Yasunishi,A., Yoshida,R., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URI: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details.
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in RIKEN contributed to prepare mouse tissues. First strand cDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGAGTCGAGTAAATTAATTAACCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.	
HOST:	SOLR
FEATURES	Location/Qualifiers
source	<p>1. . 2696          /organism="Mus musculus"          /strain="C57BL/6J"          /db_xref="MGI:MGI_1896093"          /db_xref="taxon:0090"          /clone="2810054N23"          /clone_libraries="RIKEN full-length enriched mouse cDNA library"          /dev_stage="10, 11 days embryo"          112..1524          /gene="Traip"          112..1524          /gene="Traip"          /note="Traip interacting protein          data source:MGD, source key:MGI:1096377, evidence:ISS          putative"          /acodon_start-1          /protein_id=BAB205067..1"          /db_xref="GI:12850019"          /translation="MPIRALCTICSDFFDHSRDVAATHCGHFPFLQLIQWETAPSR          TCPOCRIGVKITINKLIPDQAQEEVNLDEFLKNEFLDSKAQSKDRKRSQA          IDOTURDLEERNRNVESELQNLANKAEMLCKMLSTKMLFQFLRQDKEKARHRIK          CKMKTQEJELLIQSRSREVERMIRDMGYQGSQAVEQAVYCISLSKKEVENLFEARKAT          GEADLRKLDSVSSRKLTNLDFDKLERSAQSKQLOQSADEOETSLRKUMLQG          TSLPPNETVSRLVEPSPVEMMPRPFQEDIDUNTPPQTSQG          HCLPKKLGKLERASPSQWNLKVHKVSKPESQSLGGORCVSEBDELLELAGAPLFIRN          AVLGQKQPNTTAESRCSTDVVRIGFDGIGGRKFQPRDTTIRPVVPVSKAKSKOK</p>

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ORIGIN

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Matches	1939	Conservative	0			Gaps	3
Db	2	AAGTGTGGGTGGAGGAATTGAGAACCGACGGAGCGTGGCCGTTGGGCCAACAC	61				
Qy	62	TGTGTTGCTCTGTCAGCTGGTTCCTGGCTCTGTGTCAGTGCAGCCATCATGCCTATCC	121				
Db	62	TGTGTTGCTGCTGGCTGGAGCTGGTTCCTGGCTCTGTGTCAGTGCAGCCATCATGCCTATCC	121				
Qy	122	TCTCTCTGTCAGCTATCCTCCACTCTTGTGATCACTCCGAGCGGGTGCCATCC	181				
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Qy	542	AGGGCAGGATGAGACCAACAGCTGGGGCCACCGACTCAAGTCAGTCAGA	601				
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Qy	602	AAACCATGGAGCAATTGAGCTCTACTCAGACAGCCAGGGTTGAGGATGA	661				
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Qy	662	TTCCAGACATGGGTGGACAGTCAGCGTGGCTCTAGGAGCAAGTGA	721				
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Qy	842	ATCAGGCCAGTAGACCTGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG	901				
Db	842	ATCAGGCCAGTAGACCTGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG	901				



Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGGAGGAGGATCCAGACTCTTCTTTTTTTVN 3'], cDNA was synthesized by using triphospho-temperately-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGGAGGATCCGAGTTAAATTAAACCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

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 /strain="C57BL/6J"  
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 BASE COUNT 506 a 486 c 527 g 419 t  
 ORIGIN  
 Query Match 95.5%; Score 1886.2; DB 11; Length 1938;  
 Best Local Similarity 99.3%; Pred. NO: 0;  
 Matches 1926; Conservative 0; Mismatches 8; Indels 5; Gaps 3;  
 QY 21 GAAMTTGAGGAACCGGAGCCGGGGCGGT --CCACCAAACTGTGCTCTGCTCGC 77  
 1 GARAAUTGAGGAACCGGAGCGGGTGCGCGGTGCGGCCAACAACTGTGCTGCTCGC 60  
 QY 78 AGCTGGTTCCTGGCTGTGACTGCACCATATGCCATCTCTCTCTGTGCACTAT 137  
 61 AGCGUGTTCTGGGCTGTGACTGCACCATATGCCATCGCTATCGCGCTCTGGCACAT 120  
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BASE COUNT	251	a	219	c	245	g	171	t	others
QY	1517 GTCAGTGAAACGGTGACCAAGAGTGATGTTGCAATTAGCAGGCCAAGACCTGGCTAACCG	1576							
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QY	1757 TGGACTCTCTTGTGTTTAAAGACAGGGTACATGACTCTAAGTGGGAGTGCG	1816							
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ORGANISM	Homo sapiens								
LOCUS	AL560912								
DEFINITION	AL560912 LTI_NFL010_BC2	887 bp	mRNA	linear	EST	16-FEB-2001			
PRIMSEQ	Homo sapiens cDNA clone CS0DL005Y108	5							
ACCESSION	AL560912								
VERSION	AL560912.1								
KEYWORDS	EST.								
SOURCE	human.								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 887)								
AUTHORS	L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.								
TITLE	Full-length cDNA libraries and normalization								
JOURNAL	Unpublished (2001)								
COMMENT	Contact: Genoscope								
Genoscope - Centre National de Séquençage									
Bp 191 91006 EVRY cedex - France									
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.									
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RESULT	4								
LOCUS	AL560947								

	DEFINITION	A1560947_LTI_NFL010_BC2	Homo sapiens	cDNA clone CS0DL005Ym09	5
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	VERSION	A1560947.1		GI:12907896	
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	SOURCE	human.			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 959)				
AUTHORS	L.I.W.B., Gruber,C., Jesse,J. and Polayes,D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope				
	Genoscope - Centre National de Séquençage				
	Email: sequre@genoscope.cns.fr , Web : www.genoscope.cns.fr.				
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BASE COUNT	259 a 237 c 275 g 185 t				
ORIGIN	3 others				
Query Match	33.9%	Score 669.2;	DB 9;	Length 959;	
Best Local Similarity	85.0%	Pred. No. 3.6e-128;			
Matches	768;	Conservative	3;	Mismatches 131;	
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Qy	81 TGGATCCCGGGCGCTGAGTCAGGCCATCAGCTCATCTCTCTGCACTATCG	140			
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Qy	141 CTCGCACTTCTCGATCACTCCCGGACTGGCGCATCCACTGTGGCACATTCA	200			
Db	CTCGCACTTCTCGATCACTCCCGGACTGGCGCATCCACTGTGGCACATTCA	176			
Qy	201 TCTGCAATGCTTAATCCAGTGAGACAGCAGAACGCTGCGACCTGTGAG	260			
Db	TCTGCAATGCTTAATCCAGTGAGACAGCAGAACGCTGCGACCTGTGAG	236			
Qy	261 AATCCAGTTGGCAAAGACTTAATAACAACTTCTTGACCTCGCCAGGAA	320			
Db	AATCCAGTTGGCAAAGACCATPATCATATAAGCTCTCTTGATCTTGCCAGGAA	296			
Qy	321 GGAGAATGCTTGGATGCGAACTTAAAGAATGAATGGAGRGCGCTCAAGSCTCAGCT	380			
Db	GGAGAATGCTTGGATGCGAACTTAAAGAATGAATGGAGRGCGCTCAAGSCTCAGCT	356			
Qy	381 TTCCCGAGAACGAGGAGAACGGGACAGCCAGGCCATTAGCAGACTCTAGGGACAC	440			
Db	TTCCCGAGAACGAGGAGAACGGGACAGCCAGGCCATTAGCAGACTCTAGGGACAC	416			
Qy	441 CCTGAGAACGAGGAGAACGGGACAGCCAGGCCATTAGCAGACTCTAGGGACAC	500			
Db	CCTGAGAACGAGGAGAACGGGACAGCCAGGCCATTAGCAGACTCTAGGGACAC	476			
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REFERENCE	1	(bases 1 to 687)
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgbps-r@mail.nih.gov	
COMMENT	This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:460931 Seq Primer: -40RP from 3bco	
Query Match	32.5%	Score 641.2; DB 10; Length 702;
Best Local Similarity	98.5%; Pred. No. 2.3e-122;	
Matches	668; Conservative 0; Mismatches 8;	
LOCUS	53	CCACCAAACCTGCTGCTCTGGAGCTGTTCTGGCTGCTGAGCGGCATCA
DEFINITION	TGCCATTCCTCTCTCTGACTATCTGCTCCGACTCTCTGAGCTGAGCTGAGCTCA	112
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PROTEIN	73	TGCCATTCCTCTCTGACTATCTGCTCCGACTCTCTGAGCTGAGCTGAGCTGAGCTCA
VERSION	BF658170	CCACCAAACCTGCTGCTCTGGAGCTGTTCTGGCTGCTGAGCGGCATCA
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SOURCE	house mouse.	CTGCCATTCCTCTCTGACTATCTGCTCCGACTCTCTGAGCTGAGCTGAGCTCA
ORGANISM	Mus musculus	172
ACCESSION	BF658170	TGCCATTCCTCTCTGACTATCTGCTCCGACTCTCTGAGCTGAGCTGAGCTGAGCTCA
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KEYWORD	EST.	CTGCCATTCCTCTCTGACTATCTGCTCCGACTCTCTGAGCTGAGCTGAGCTGAGCTCA
SOURCE	house mouse.	192
ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Sciuromorpha; Muridae; Murine; Mus; Eutheria; Rodentia	173
RESULT	6	CTGCCATTCCTCTCTGACTATCTGCTCCGACTCTCTGAGCTGAGCTGAGCTGAGCTCA
BASE COUNT	186	193
ORIGIN	a	CACCAAGTCGACGCCAGCTGAGAATCCAGTGTAGATCCAGGTGGCAAAGACATTATAAACAA
BASE COUNT	175	232
ORIGIN	c	CTGCCATTCCTCTCTGACTATCTGCTCCGACTCTCTGAGCTGAGCTGAGCTGAGCTCA
BASE COUNT	182	252
ORIGIN	g	353 ATGAAGCTGGCAGCGCTCAAGCTCACTTCAGTGGAAAGCAGGGAGAACGGGAGCAGC
BASE COUNT	144	352
ORIGIN	t	313 ATGAAGCTGGCAGCGTC-AAGCTCACTTTCAGAAGAGGAGAACAGGGAGCACGCC
BASE COUNT	186	371
ORIGIN	a	413 AGGCCATTATGACACTCTACGGGACACCTTGAGAAGACGGCATGTACCGTGGAGTCCC
BASE COUNT	175	472
ORIGIN	c	372 AGGCCATTATGACACTCTACGGGACACCTTGAGAAGACGGCATGTACCGTGGAGTCCC
BASE COUNT	182	431
ORIGIN	g	473 TACAGAACCGCTTAACAACAGCAGATGGTGTGTTCCACCTGAAAAAACAGATAAGT
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ORIGIN	t	432 TACAGAACCGCTTAACAACAGCAGATGGTGTGTTCCACCTGAAAAAACAGATAAGT
BASE COUNT	186	491
ORIGIN	a	533 TCCTTGAGCAGCGGAGGAGGAGGAGACAAACAGCTGGGGAGGCCACGGACTCAACT
BASE COUNT	175	592
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ORIGIN	g	593 GCAAGATGAAACCATTGGAGAATTTGAGCTTCTACCTGGAGGCCACAGCTGGTGTGTT
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BASE COUNT	175	611
ORIGIN	a	653 AGGAGATGATTCGAGACATGGTGTGGAC-CAGTCAGCGGAGGAGCTGGTGTGAC
BASE COUNT	144	711
ORIGIN	g	612 AGGAGATGATTCGAGACATGGTGTGGACAGTCAGCGGAGCTGGTGTGAC
BASE COUNT	186	671
ORIGIN	t	712 TGGCTGTCCCTCAAGAAA 729
BASE COUNT	144	689
ORIGIN	b	672 TGGCTGTCCCTCAAGAAA 689
RESULT	6	BF658170
BASE COUNT	186	687
ORIGIN	a	687 bp mRNA linear EST 20-DEC-2000
DEFINITION	ma96b06.Y1 Soares-thymus 20Nb7 Mus musculus cDNA clone	
IMAGE	3824579	5' similar to TR:008854 008854 TRAF-INTERACTING
PROTEIN	; mRNA sequence.	
ACCESSION	BF658170	
VERSION	BF658170.1	GR:11923304
KEYWORD	EST.	
SOURCE	house mouse.	
ORGANISM	Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murine; Mus.	
RESULT	6	QY100001
BASE COUNT	186	687
ORIGIN	a	687 bp mRNA linear EST 20-DEC-2000
DEFINITION	ma96b06.Y1 Soares-thymus 20Nb7 Mus musculus cDNA clone	
IMAGE	3824579	5' similar to TR:008854 008854 TRAF-INTERACTING
PROTEIN	; mRNA sequence.	
ACCESSION	BF658170	
VERSION	BF658170.1	GR:11923304
KEYWORD	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	6	QY100001
BASE COUNT	186	687
ORIGIN	a	687 bp mRNA linear EST 20-DEC-2000
DEFINITION	ma96b06.Y1 Soares-thymus 20Nb7 Mus musculus cDNA clone	
IMAGE	3824579	5' similar to TR:008854 008854 TRAF-INTERACTING
PROTEIN	; mRNA sequence.	
ACCESSION	BF658170	
VERSION	BF658170.1	GR:11923304
KEYWORD	EST.	
SOURCE	house mouse.	
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BASE COUNT	186	687
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ORGANISM	Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murine; Mus.	
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IMAGE	3824579	5' similar to TR:008854 008854 TRAF-INTERACTING
PROTEIN	; mRNA sequence.	
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VERSION	BF658170.1	GR:11923304
KEYWORD	EST.	
SOURCE	house mouse.	</

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Db	481	GAGATGCTGTGTTACCCGAAACAGATGAGAAGTTCCTGGAGCAGGGAGGATGAG	540
QY	556	ACCAACAGCTGGGGAGGCCAACCGACTCAAGTGCAAGATGAAACCATGGAGCA	615
Db	541	ACCAACAGCTGGGGAGGCCAACCGACTCAAGTGCAAGATGAAACCATGGAGCA	600
QY	616	ATTGAGCTCTACTCCAGAGGCAGGCTCTGGTGAGGAGATGATTCAGACATGGT	675
Db	601	ATTGAGCTCTACTCCAGAGGCAGGCTCTGGTGAGGAGATGATTCAGACATGGT	660
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DEFINITION	BF162255	601770948P1 NCI_CGAP_Lu29 744 bp mRNA linear EST 30-OCT-2000	
mRNA sequence.			
ACCESSION	BF162255		
VERSION	BF162255.1		
KEYWORDS	EST.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurographi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 744)		
AUTHORS	NIH_MGC http://mgc.ncbi.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: ccrapsb-r@mail.nih.gov CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLNL9201 row: o column: 12		
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	/clone="IMAGE:3990371"		
	/clone_lib="NCI_CGAP_Lu29"		
	/tissue_type="spontaneous tumor, metastatic to mammary."		
	/stem_cell_origin=" "		
	/lab_host="DH10B"		
	/note="Organ: lung; Vector: PCMV-SPORT5; Site:1: Sali; Site:2: NotI; Cloned unidirectionally. Primer: oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	201 a 183 c 212 g 148 t		
ORIGIN			
RESULT	8		
LOCUS	BM464844		
DEFINITION	AGENCOURT_642861 NIH_MGC_85 Homo sapiens	1061 bp mRNA	linear EST 05-FEB-2000
mRNA sequence.			
ACCESSION	BM464844	5'	
VERSION	BM464844.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1061)		
AUTHORS	NIH_MGC http://mgc.ncbi.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: ccrapsb-r@mail.nih.gov CDNA Library Preparation: Lou Staudt DNA Sequencing by: Agenourt Bioscience Corporation (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLNL12147 row: b column: 19		
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Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744;		
Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
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Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
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Best Local Similarity	96.3%; Pred. No. 1.4e-120;		
Matches	702; Conservative 0; Mismatches 19; Indels 8; Gaps 5;		
ORIGIN			
Query Match	32.9%; Score 632.6; DB 10; Length 744		



Db	240	CCAGGCCAACGCTGGATACCTCTTGTCACTGAGTCAGCAGCGAGACTCAGTTGCAA	299
QY	1551	TAGTGGCCCAAGACCTGGCTAACCGGAAGTGTGTTGGAAAGATGGCTCCCTGGACCAG	1610
Db	300	TAGTGGCCCAAGACCTGGCTAACCGGAAGTGTGTTGGAAAGATGGCTCCCTGGACCAG	358
QY	1611	TCCAAGAGAGTGCCCCGAAACACACTTCCGCTGTCACAGCGCCCTGCACACACTGG	1670
Db	359	TCCAAGAGAGTGCCCCGAAACACACTTCCGCTGTCACAGCGCCCTGCACACACTGG	418
QY	1671	G-AAGCCACATGACCAGTTACTGTCGATCAGCAGGGCTACTCCAGTGCAGGGT	1729
Db	419	GAAAGCCACATGACCAGTTACTGTCGATCAGCAGGGCTACTCCAGTGCAGGGT	478
QY	1730	TGCTCATAGCTACAACCAGGNGGCTGACTCCTTGTGTTATAGAACAGGGTCAC	1789
Db	479	TGCTCATAGCTACAACCAGGNGGCTGACTCCTTGTGTTATAGAACAGGGTCAC	538
QY	1790	ATGACTCTAAGTGGATGGAGTGTGAGGATCTATGAGCTGAGGTGAGCTGAGGT	1849
Db	539	ATGACTCTAAGTGGATGGAGTGTGAGGATCTATGAGCTGAGGTGAGCTGAGGT	598
QY	1850	TGACTCTG 1859	
Db	599	TGACTCTG 608	
RESULT	10		
LOCUS	BE334637	BE334637 589 bp mRNA linear EST 14-JUL-2000	
DEFINITION	us81912..Y1 NCI-CGAP_Mana4	Mus musculus cDNA clone IMAGE:325f638 5'	
REFERENCE	1 (bases 1 to 589)	similar to TR:008854 008854 TRAF-INTERACTING PROTEIN ; mRNA	
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
Ph.D.	Email: cgaps@mail.nih.gov		
Tissue	Procurement: Lothar Hennighausen Ph.D., Priscilla Furth		
CDNA	Library Preparation: Life Technologies, Inc.		
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)		
Clone	Sequencing by: Washington University Genome Sequencing Center		
found through the I.M.A.G.E. Consortium/ILNL at:	image.lnl.gov/image/html/resources.shtml		
MGI:1069002			
Seq primer:	-40RP from Gibco		
FEATURES	High quality sequence stop: 362.		
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	/db_xref="txid:10990"		
	/clone="IMAGE:325f638"		
	/clone_id="NCI-CGAP_Mana4"		
	/tissue_type="tumor", gross tissue"		
	/dev_stage="5 months,"		
	/lab_host="DH10B"		
	/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;		
	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.		
	Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth,		
BASE COUNT	152	a 151 c	172 g 114 t
ORIGIN			
Query Match	27.3%	Score 539; DB 10;	Length 589;
Best Local Similarity	97.8%	Pred. No. 3e-101;	
Matches	578;	Conservative 0;	Mismatches 10;
		Indels 3;	Gaps 3;
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 589)		
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
RESULT	11		
LOCUS	AA684194	AA684194 554 bp mRNA linear EST 09-DEC-1997	
DEFINITION	vm68d10.s1 Knowles_Solter mouse 2 cell Mus musculus cDNA clone IMAGE:10034115	similar to TR:008854 008854 MTRIP. ; mRNA	
SEQUENCE	AA684194		
ACCESSION			
VERSION	AA684194.1	GT:2670780	
KEYWORDS			
SOURCE			
ORGANISM			
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 554)		
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubreuil,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheibenbogen,K., Stoebe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
TITLE	The WashU HMM Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project		



Best Local Similarity 84.5%; Pred. No. 5.2e 96%; Matches 612; Conservative 0; Mismatches 109; Indels 3; Gaps 3;

Db	282	GAGAAATGTCCTGGATCGAGATTCATAAGGATGACTGACAAATGTCAGGCCAGT	341
Qy	381	TCCCCAGAACGACGGAGAACGGCACGCCAGGCATTATCGACACTCTACGGGAC	440
Db	342	TCCCCAGAACGACGGAGAACGGCACGCCAGGCATTATCGACACTCTACGGGAC	401
Qy	441	CCTGGAGAACGCAATGCTACGGGAGTCAGAAGCCTAACAGAGAGAT	500
Db	402	GCTGGAGAACGCAATGCTACGGGAGTCAGAAGCCTAACAGAGAGAT	461
Qy	501	GCTGTCTCCACCTGAAGAACAGATGAATGTTCTGGAGCAGGCCAGT	560
Db	462	GCTGTCTCCACCTGAAGAACAGATGAATGTTCTGGAGCAGGCCAGT	521
Qy	561	ACAACTCGGGAGGGGCCACCGACTAAGTCAGATGAAACCATGAGCAA	620
Db	522	ACAACTCGGGAGGGGCCACCGACTAAGTCAGATGAAACCATGAGCAA	581
RESULT	13		
BG682548			
LOCUS	BG682548	752 bp mRNA linear EST 01-MAY-2001	
DEFINITION	60362432F1 NCI_CGAP_Skn4	Homo sapiens cDNA clone IMAGE:4749475', mRNA sequence.	
ACCESSION	582	GCTCTTAATCGCAGGCCGCGGAGGAGACGATCGAGACATGGGTG	641
Qy	680	GACAGTCAGGGGGAGCACGGCTGGTGTRACTGGTGCTCCAGAAGAGATG	736
Db	642	GACAGACAGGGGGAGCACGGCTGGTGTRACTGGTGCTCCAGAAGAGATG	698
SOURCE			
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE			
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.	
VERSION	BG682548.1	GI:13913945	
KEYWORDS	EST.		
COMMENT			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
CONTACT	Robert Strausberg, Ph.D.		
EMAIL	cgbps-r@mail.nih.gov		
Tissue Procurement:	James Cleaver, M.D.		
CDNA Library Preparation:	Life Technologies, Inc.		
CDNA Library Arrayed by:	the T.M.A.G.E. Consortium (LLNL)		
DNA Sequencing by:	Incyte Genomics, Inc.		
Clone distribution:	MGC clone distribution information can be found through the T.M.A.G.E. Consortium at: http://image.llnl.gov		
Plate:	LIAM10602 row: k column: 16		
High quality sequence start: 19			
High quality sequence stop: 736.			
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:474947"		
	/tissue_type="squamous cell carcinoma"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: skin; vector: pCMV-SPOR6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."		
BASE COUNT	200 a 194 C 212 G 146 T		
ORIGIN			
Query Match		26.0%; Score 513.6; DB 10; Length 752;	
RESULT	14		
B301189			
LOCUS	B304199	519 bp mRNA linear EST 13-JUL-2000	
DEFINITION	60108621F1 NCI_CGAP_Mam6	Mus musculus cDNA clone IMAGE:35008215', mRNA sequence.	
ACCESSION	B304199		
VERSION	B304199.1	GI:9174333	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE			
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Contact: Robert Strausberg, Ph.D.		

DEFINITION		602347389F1 NIH_MGC_90	Homo sapiens	CDNA clone IMAGE:442038 5'
FEATURES	source	mRNA sequence.		
1. .519		http://image.llnl.gov		
Plate: LLAM059	row: 1 column: 06	Plate: LLAM059		
High quality sequence stop: 515.		High quality sequence stop: 515.		
Location/Qualifiers				
1. .519				
Query Match				
Best Local Similarity	26.0%	score 513.4; DB 10; Length 519;		
Matches	514; Conservative	Pred. No. 6e-96; 0; Mismatches 1; Indels 0; Gaps 0;		
QY	263	TCCAGGTGGCAAAAGACTATTATAAACCAACTTTCCTTGACCTCGCCAGGAAGAGG 322		
Db	5	TCCAGGTGGCAAAAGACTATTATAAACCAACTTTCCTTGACCTCGCCAGGAAGAGG 64		
QY	323	AGAATGTCCTGGTGGAGAATCTTCTTAAAGATACTGGAGCAGGTCAAAGCTCAAGTT 382		
Db	65	AGAATGTCCTGGTGGAGAATCTTAAAGATACTGGAGCAGGTCAAAGCTCAAGTT 124		
QY	383	CCCGAAAGCAGGGAAACGGGACGCCAGGGCATATGACACTCTACGGACACC 442		
Db	125	CCCGAAAGCAGGGAAACGGGACGCCAGGGCATATGACACTCTACGGACACC 184		
QY	443	TGGAAGAACCAATGCTACCGCTGGAGCTCCCTACAGAACGCCCTTAACAAAGCAGAGTC 502		
Db	185	TGGAGAACCCATGCTACCGCTGGAGCTCCCTACAGAACGCCCTTAACAAAGCAGAGTC 244		
QY	503	TGTGTTCCACCTGTGAAAACAGAGTGAAGTCTGGAGCACGGCAGGAGTAGACCAAAC 562		
Db	245	TGTGTTCCACCTGTGAAAACAGAGTGAAGTCTGGAGCACGGCAGGAGAACCAAC 304		
QY	563	AGCTCGGGAGGCCACGACTCAAGTCAGAATGAAACCATGGCAATTGAGC 622		
Db	305	AAGCTCGGGAGGCCACGACTCAAGTCAGAATGAAACCATGGCAATTGAGC 364		
QY	623	TCTACTCCAGAGCCAGCGTCTGTGAGGTGGAGGAGTGTGAGACATGGTGGAC 682		
Db	365	TCTACTCCAGAGCCAGCGTCTGTGAGGTGGAGGAGTGTGAGACATGGTGGAC 424		
QY	743	TGAAGGAGGTGGAGGCCACAGGGAACTGGCT 777		
Db	485	TGAAGGAGGTGGAGGCCACAGGGAACTGGCT 519		
BASE COUNT	159 a	116 c	152 g	92 t
ORIGIN				
REFERENCE		1 (bases 1 to 784)		
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/		
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov		
Tissue Procurement: ARCC				
cDNA Library Preparation: Life Technologies, Inc.				
DNA Sequencing by: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
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Location/Qualifiers				
1. .784				
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Best Local Similarity	25.9%	score 510.6; DB 10; Length 784;		
Matches	594; Conservative	Pred. No. 2.2e-95; 0; Mismatches 84; Indels 3; Gaps 0;		
QY	81	TGGTTCCCTGGGCCTGCTGAGTCAGTCAGCCATCATGCCCTACGTGCTCTGCACTATCG 140		
Db	62	TGGCTCCCTGGGCCTGAGTCAGCCATCATGCCCTACGTGCTCTGCACTATCG 121		
QY	141	CTCGCACTCTTGATCACTCCGGTACGTGGCTGCCATCAGCTGGCACACTTICA 200		
Db	122	CTCGCACTCTTGATCACTCCGGTACGTGGCTGCCATCAGCTGGCACACTTICA 181		
QY	201	TCTGCAATGCTTAATCCAGTGGTTGAGACAGCACCAAGCTGGCACAGTGTAG 260		
Db	182	CTTGCACTCTTGATCACTCCGGTACGTGGCTGCCATCAGCTGGCACACTTICA 241		
QY	261	AATTCGAGTTGGCAAAAGACTATATAAACACACTTTCCTTGACCTGGCCAGGAAGA 320		
Db	242	AATTCGAGTTGGCAAAAGACCATTTATCATATAAGCTTGCCCTTGCCAGGAGGA 301		
QY	321	GGAGATGCTTGTGAGCAATCTTAAGAGTGAACGTGGACAGCGCTAACCTCAGT 380		
Db	302	GGAGATGCTTGTGAGCAATCTTAAGAGTGAACGTGGACATGTGAGGCCAGCT 361		
QY	381	TCTCCAGAAAGCAGGGAAACGGGACGCCAGGGCAATTATCGACACTCTACGGACAC 440		
Db	362	TCTCCAGAAAGCAGGGAAACGGGACGCCAGGGCAATTATCGACACTCTACGGACAC 421		
QY	441	CCTGGAGAACGCAATGCTACCGTGGAGTCAGCCCTACAGAACGCCCTAACAGGGAGAT 500		
Db	422	GCTGGAGAACGCAATGCTACCGTGGAGTCAGCCCTACAGAACGCCCTAACAGGGAGAT 481		
RESULT	15	BG120736	784 bp	mRNA linear EST 30-JAN-2001
LOCUS		BG120736		

QY 501 GCTGCGTTCCACCCGTAAAGAACAGATGAAGTTCCTGGACAGGGCAGGATGACCA 560  
 Db 1 GCCCCCTTGATGCCAGCCATCATGCCTATCGTGCCTCTGCACTTCCTCGACTTC 60  
 Db 482 GCTGCGCTCCACAGAAAGCAGATGAAGTCACTTGAAGCAGCACGAGGACCAA 541  
 QY 561 ACAAAGCTGGAGGGGCCACCGACTCAAGTGCAGATGAAACCATGGAGCAATGA 620  
 Db 542 ACAAAGCAAGAGGGGCC-GCGCTCAGGAGCAAGATGAAGAACCATGGAGCAATGA 600  
 QY 621 GCTCCACTCGAGGCCAGCGTCTGAGGGAGGAGATATTGAGACATGGGGTGGG 680  
 Db 601 GCTCTACTCCAGAGCCAGGCCCTGAGGAGATGATCCGAGACATGGGGTGGG 660  
 QY 681 ACAGTCAGCGGGAGGAGCAGCTGCGTGTACTGCTGTCCTCAAGAAGAGTGAAGA 740  
 Db 661 ACAGTCAGCGGGAGGAGCAGCTGCGTGTACTGCTGTCCTCCAGAAAGAGT-CGAAA 718  
 QY 741 TCTGAGGAAGCTCGGAAGGC 761  
 Db 719 TCTAAAGAAGCCGGAGGC 739

RESULT 16  
 LOCUS BG420765 908 bp mRNA linear EST 14-MAR-2001  
 DEFINITION 602448558F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4586846 5',  
 ACCESSION BG420765  
 VERSION BG420765.1 GI:13327271  
 KEYWORDS EST.  
 COMMENT human.  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 908)  
 AUTHORS NIH-MGC <http://mgc.ncbi.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 Email: cgabps-r@mail.nih.gov  
 TISSUE source  
 PROCUREMENT CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://Image.llnl.gov>  
 Plate: LCM1316 row: d column: 15  
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 /tissue\_type="renal cell adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: kidney; Vector: pCRB7; Site\_1: XbaI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT  
 ORIGIN  
 Query Match 25.5%; Score 504.2; DB 10; Length 908;  
 Best Local Similarity 82.0%; Pred. No. 4.4e-94;  
 Matches 663; Conservative 0; Mismatches 93; Indels 53; Gaps 5;  
 QY 91 GGCTGCTTGGAGCCATCATGCCTATCCTCTCTGACTATCTGCTCGACTTC 150

RESULT 17  
 LOCUS BE546959 825 bp mRNA linear EST 09-AUG-2000  
 DEFINITION 60107129F1 NIH\_MGC\_12 Homo sapiens cDNA clone IMAGE:34588023 5',  
 ACCESSION BE546959  
 VERSION BE546959.1 GI:9775604  
 KEYWORDS EST.  
 COMMENT human.  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 825)  
 AUTHORS NIH-MGC <http://mgc.ncbi.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.

	Email: cgabs-r@mail.nih.gov
	Tissue Procurement: ARCC
	CDNA Library Preparation: Life Technologies, Inc.
	CDNA Library Arrayed by: Incyte Genomics, Inc.
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov
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	High quality sequence stop: 655.
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	/tissue_type="cervical carcinoma cell line"
	/lab_host="DNI10B"
	/note="Organ: cervix; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Technologies." Average insert size 1.4 kb. Library prepared by Life
BASE COUNT	230 a 209 c 242 g 144 t
ORIGIN	
Query Match	25.5%; Score 503.2; DB 10; Length 825;
Best Local Similarity	85.1%; Pred. No. 7.2e-94;
Matches	633; Conservative 0; Mismatches 103; Indels 8; Gaps 6;
QY	135 TACCTGCTCGACATCTTGATCACTCCCGTGACTGGCTGCCATCCACTGTGGCACAC 194
Db	1 TAATCAGTCGCGACATCTTGATCACTCCCGTGACTGGCTGCCATCCACTGTGGCACAC 60
QY	195 TTTCATCGCATGCCATGCCATATCCAGTGGTTGAGACAGGCCAGTCGGACCAGCCCACA 254
Db	61 CTTCCACTTGCACTGGCTTAATTCACTGTGGACAGGCCAGTCGGACCAGCCCACA 120
QY	255 GTGTTAGAACCTCAGGGTGGCAAARAGACTATATAACAACTTCTTGACCTGGCGCCA 314
Db	121 GTGCCGAATCCAGGTGGCAAAAGAACATTATCAATAAGCTCTCTTGATCTGGCCA 180
QY	315 GGAGGAGGAAAGTCTTGATSGAGAATCTTAAGATGACTGGACAGCCAAAGC 374
Db	181 GGAGGAGGAAATGTTGATGCGAAATCTTAAGAATGACTGGACATGGCAATGAGCAGGC 240
QY	375 TAGCTTCCAGAAAGACAGGGAGACGGGAGCAGGCCATTATGACACTCTAG 434
Db	241 CCAGCTTCCAGAAAGACAGGGAGACAGGCCATTATGACACTCTAG 300
QY	435 GGACACCCCTGGAGAACGCAATGCCATACGGTGTCTCGCGCAGGCCCTAACAGGC 494
Db	301 GGATACGCTGGAGAACGCAATGCTACTGTGGATCTCGCGCAGGCCCTGGCAAGGC 360
QY	495 AGAGATGCGTGTGTCACCCGTGAAAGAGAGAAGTGTCTCGCGCAGGCCAGGAGCA 554
Db	361 CGAGATGCTGTGTCACACTGAAAGCAGATGAGTACTTACAGCAGCAGGATGA 420
QY	555 GACCAACAGCTGGAGGAGGCCACGGACATCACTGGCAAGATGAAACCATGGCA 614
Db	421 GACCAACAGCAAGAGGCCACGGACATCACTGGCAAGATGAAACCATGGCA 480
QY	615 ATTAGAGCTCTACTCCAGGCCACGGCTCTGAGGTGGAGGAGATGCGAGCATGG 674
Db	481 GA-TGAGCTCTACTCCAGGCCACGGCTCTGAGGTGGAGGAGATGCGAGCATGG 539
QY	675 TGTGGACAGCTGGAGGAGCTGGACTGTGACTGGCTGGAGGAGCTGGAGGAG 733
Db	540 TGTGGACAGCTGGAGGAGCTGGCTGTGACTGTGCTCTGAGGAG 599
QY	734 ATGAAATCTGAGGAAGCTGGAGGCCACAGGGAACTGCTGACAGGTGAGAAG 792
Db	600 ACGGAATCTAAAGAGGCAAGGCCACGGCTCCAGGAGGGTGGTACAGCTGAGGAAG 659
RESULT	18
LOCUS	AL559248
DEFINITION	AL559248_LTR-NFL008_TC2 Homo sapiens cDNA clone CSODJ012YH21
PRIMERS	prime, mRNA sequence.
ACCESSION	AL559248
VERSION	AL559248.1
KEYWORDS	EST
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	I. (bases 1 to 65)
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Centre National de Séquençage
FEATURES source	Location/Qualifiers
	1. . 645
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="CS0Dj012YH21"
	/clone_libr="LTL_NFL008_TC2"
	/sex="male"
	/tissue_type="T cells from T cell leukemia"
	/note="Vector: pcMVSport 6; Site_1: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSport 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetechnologies.com URL : http://fulllength.invitrogen.com"
BASE COUNT	167 a 174 c 177 g 127 t
ORIGIN	
Query Match	25.2%; Score 497.4; DB 9; Length 645;
Best Local Similarity	88.4%; Pred. No. 1.2e-92;
Matches	540; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY	81 TGGTGCCTGGCTCTTGAGTCGAGCCATCATGCCCTATCTCTCTCTGACTATCTG 140
Db	35 TGGCTGCCCTGGGCCCTCTGAGTCGAGCCATCATGCCCTATCTGACTATCTG 94
QY	141 CTGGCACTCTTGTGATCACTCCGGTGGACCTGGCTGCCATCTGACTGTGCTGG 200
Db	95 CTGGCACTCTTGTGATCACTCCGGTGGACCTGGCTGCCATCTGACTGTGCTGG 154
QY	201 TCTGCAATGCCCTAATCTGGTGGAGGAGCTGGCTGCCACAGTGAG 260
Db	155 CTGGAGTGTGCTTAATCTGGAGGAGCTGGCTGCCACAGTGAG 214
QY	261 AATCCAGGTGGCAAAAGACTATATAACAACTTCTTCTGACTGCCCCAGGAAGCA 320
Db	215 AATCCAGGTGGCAAAAGAACATTATCAATAAGCTCTCTTGTGCTGCCACAGGAGGA 274
QY	321 GGAGATGTCTGGATGCGAATCTTAAGAATGAACTGGACAGCGTCAAAGCTCAGGT 380



TITLE	
JOURNAL	
COMMENT	
Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: Life Technologies, Inc.	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam1503 row: 1 column: 19	
High quality sequence stop: 666.	
Location/Qualifiers	
1. . 668	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:5200986"	
/clone.lib="NIH MGC_114"	
/clone.host="DH10B"	
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."	
BASE COUNT	
174 a	178 c
ORIGIN	
178 g 129 t	
Query Match	
Best Local Similarity	24.8%
Matches	533;
Conservative	0;
Mismatches	71;
Indels	0;
Gaps	0;
Length 668;	
Score 490.4;	
DB 10;	
LOCUS	
BB889971	BB889971 NIH MGC_71 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889971
VERSION	BB889971.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_71"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	
BASE COUNT	
279 a	259 c
ORIGIN	
289 g 156 t	
Query Match	
Best Local Similarity	24.5%
Matches	579;
Conservative	0;
Mismatches	103;
Indels	3;
Gaps	3;
Length 983;	
Score 484.2;	
DB 10;	
LOCUS	
BB889972	BB889972 NIH MGC_72 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889972
VERSION	BB889972.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_72"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	
BASE COUNT	
279 a	259 c
ORIGIN	
289 g 156 t	
Query Match	
Best Local Similarity	24.5%
Matches	579;
Conservative	0;
Mismatches	103;
Indels	3;
Gaps	3;
Length 983;	
Score 484.2;	
DB 10;	
LOCUS	
BB889973	BB889973 NIH MGC_73 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889973
VERSION	BB889973.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_73"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	
BASE COUNT	
279 a	259 c
ORIGIN	
289 g 156 t	
Query Match	
Best Local Similarity	24.5%
Matches	579;
Conservative	0;
Mismatches	103;
Indels	3;
Gaps	3;
Length 983;	
Score 484.2;	
DB 10;	
LOCUS	
BB889974	BB889974 NIH MGC_74 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889974
VERSION	BB889974.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_74"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	
BASE COUNT	
279 a	259 c
ORIGIN	
289 g 156 t	
Query Match	
Best Local Similarity	24.5%
Matches	579;
Conservative	0;
Mismatches	103;
Indels	3;
Gaps	3;
Length 983;	
Score 484.2;	
DB 10;	
LOCUS	
BB889975	BB889975 NIH MGC_75 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889975
VERSION	BB889975.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_75"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	
BASE COUNT	
279 a	259 c
ORIGIN	
289 g 156 t	
Query Match	
Best Local Similarity	24.5%
Matches	579;
Conservative	0;
Mismatches	103;
Indels	3;
Gaps	3;
Length 983;	
Score 484.2;	
DB 10;	
LOCUS	
BB889976	BB889976 NIH MGC_76 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889976
VERSION	BB889976.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_76"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	
BASE COUNT	
279 a	259 c
ORIGIN	
289 g 156 t	
Query Match	
Best Local Similarity	24.5%
Matches	579;
Conservative	0;
Mismatches	103;
Indels	3;
Gaps	3;
Length 983;	
Score 484.2;	
DB 10;	
LOCUS	
BB889977	BB889977 NIH MGC_77 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889977
VERSION	BB889977.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_77"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	
BASE COUNT	
279 a	259 c
ORIGIN	
289 g 156 t	
Query Match	
Best Local Similarity	24.5%
Matches	579;
Conservative	0;
Mismatches	103;
Indels	3;
Gaps	3;
Length 983;	
Score 484.2;	
DB 10;	
LOCUS	
BB889978	BB889978 NIH MGC_78 Homo sapiens mRNA
DEFINITION	983 bp linear IMAGE:3113854 5'
ACCESSION	BB889978
VERSION	BB889978.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 983)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.lnl.gov	
Plate: Llam9734 row: k column: 07	
High quality sequence stop: 664.	
Location/Qualifiers	
1. . 983	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3913854"	
/clone.lib="NIH MGC_78"	
/clone.host="DH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
Average insert size 1.5 kb."	

		BASE COUNT	163 a	171 c	172 g	126 t
Db	303	GGAGAATGTTGGATGCAGAAATTAAAGAATGAACTGGACATGTGAGGCCAGT	362			
Qy	381	TCCCCAGAACAGAACGGAGAACGGACAGCCGCAATATCGACACTCTACGGACAC	440			
Db	363	TCCCCAGAACAGAACGGAGAACGGACAGCAGCCGGTCATCATCGACACTCTCGCGGATC	422			
Qy	441	CCTGAAAGAACGCAATGCTACCGTGAGTCCTACAGAACGCCATTATCGACACTCTACGGACAC	500			
Db	423	GCTGGAGAACGCAATGCTACCGTGAGTCCTACAGAACGCCATTATCGACACTCTCGCGGATC	482			
Qy	501	GCTGTTCCACCTGAAGAACAGATGAGTCCTGGACCGAGCCAGGGCAGATGAGCA	560			
Db	483	GCTGTTCTCACAGAACAGATGAGTCCTAGACGAGGAGATGAGCA	542			
Qy	561	ACAACTCGGGAGGGCCACCGACTCAAGTGAAGAACATGGACAAATTGA	620			
Db	543	ACAGCACAGAGGGCCGCCGCTCAGGAGAACATGGAGAGATGA	602			
Qy	621	GCTCTACTCCAGAACGGCCAGCTGAGTGGAGAGATGAGTCGAG-ACATGGTGG	679			
Db	603	GCTCTACTCCAGAACGGCCAGCTGAGTGGAGAGATGAGTCGAGACATGGTGG	651			
Qy	680	GACAGTCAGGGTGGAGCAGTGGCTGT-TACTGCCTCCCTCAAGAACAGATGAG	738			
Db	662	GACAGTCAGGGAACCCGCTGCTGGTAAACGGGGCTCTCAAGAACGGTCCAA	721			
Qy	739	AATCTGAAGGAAGCTGGAGGCCA	763			
Db	722	AATCCTAACAGAGGCCAACGGTCA	746			
RESULT	22					
BF219707						
LOCUS	BF219707	632 bp mRNA linear EST 08-NOV-2000				
DEFINITION	601296327F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821007 5'					
ACCESSION	BF219707					
VERSION	BF219707.1					
KEYWORDS	EST					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 to 632					
TITLE	NIH-MGC <a href="http://mgc.ncbi.nih.gov/">http://mgc.ncbi.nih.gov/</a>					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)					
COMMENT	Unpublished (1999)					
Contact:	Robert Strausberg, Ph.D.					
cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)					
DNA Sequencing by:	Incyte Genomics, Inc.					
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>					
Plate:	IRALI row: e column: 07					
High quality sequence stop:	630.					
FEATURES	Location/Qualifiers					
source	I.. .632					
/organism="Homo sapiens"						
/clone="IMAG3:2821007"						
/tissue_type="small cell carcinoma"						
/cell_line="MGC3"						
/lab_host="PH10B (phage-resistant)"						
/note="Organ: lung; Vector: POM7; Site_1: XbaI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adapter: GCGAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."						
RESULT	23					
BG117979						
LOCUS	BG117979	912 bp mRNA linear EST 30-JAN-2001				
DEFINITION	602351223F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:446149 5'					
ACCESSION	BG117979					
VERSION	BG117979.1					
KEYWORDS	EST					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 912)					
TITLE	NIH-MGC <a href="http://mgc.ncbi.nih.gov/">http://mgc.ncbi.nih.gov/</a>					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)					
COMMENT	Unpublished (1999)					
Contact:	Robert Strausberg, Ph.D.					
Email:	<a href="mailto:cgapbs-1@mail.nih.gov">cgapbs-1@mail.nih.gov</a>					
Tissue Procurement:	ATCC					
CDNA Library Preparation:	Life Technologies, Inc.					
DNA Sequencing by:	Incyte Genomics, Inc.					
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>					

		RESULT	24
FEATURES	source	BB821649	BB821649 row: n column: 06
High quality sequence stop:	678.	LOCUS	BB821649 528 bp mRNA linear EST 19-NOV-2001
Location/Qualifiers		DEFINITION	JYg-MCA) cDNA Mus musculus cDNA clone G830012P09 3', mRNA sequence.
1. . 912		ACCESSION	BB821649
/db_xref="txon:9606"		VERSION	BB821649.1 GI:16994278
/clone="IMAKE:446149"		KEYWORDS	EST
/clone.lib=NIH_MGC_90"		SOURCE	house mouse.
/organism="Homo sapiens"		ORGANISM	Bius musculus
/tissue_type="adenocarcinoma, cell line"		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
/lab_host="PBL10B (phase-resistant)"		REFERENCE	1 (bases 1 to 528)
/note="organ: liver; vector: pcMV-SPORT6; site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.		AUTHORS	Akimura,T., Arkawa,T., carninci,P., Furuno,M., Hanagai,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kohlma,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomasaki,R., Okazaki,T., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takao,Akira,S., Tanaka,T., Tomaru,T., Toyoda,T., Watanuki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
BASE COUNT	ORIGIN	TITLE	RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
236 a 243 c 273 g 160 t		JOURNAL	Unpublished (2001)
Query Match	23 3%	COMMENT	Contact: Yoshihide Hayashizaki
Best Local Similarity	83.8%		Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
Matches	591; Conservative 0; Mismatches 107; Indels 7; Gaps 6;		The Institute of Physical and Chemical Research (RIKEN)
QY	81 TGGTCCCCTGGCTCTTGAGTGAGCCATCATGCCATTCCTCTGTGACTATCTG 140		1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Db	65 TGGTGCCTGGGCCCTTGAGTCAGCATCATGCCATTCCTCTGTGACTATCTG 124		Tel: 81-45-503-9222
QY	141 CTGGACTCTTGTGATCACTCCCGTACGTTGACACTTCTTCA 200		Fax: 81-45-503-9216
Db	125 CTCCGACTCTTCGATCCCGACCTGGCCACCTTCCA 184		Email: genome-res@gsc.riken.go.jp/
QY	201 TCTGCAATGCCTAACTCCAGTGGTGTAGACAGACCGAACAGTCGGACCTGCCAACGTGAG 260		URL: http://genome.gsc.riken.go.jp/
Db	185 CTTGAGTAGCTTAATTCAGTGGTTGAGACAGACGACCAACTCGGACCTGCCAACGTGAG 244		Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Hayamatsu,M. and Hayashizaki,Y.
QY	261 ATTCAGGTTGGCAAAGACTATTAAACAACTTCTTGACCTGGCCAGGAGA 320		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
Db	245 ATTCAGGTTGGCAAAGACCAACTTAAAGTCACTCTCTTGATCTTGCCAGGAGA 304		wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
QY	321 GGAGAATGCTTGGATGAGAACTTAAAGATGAACTTGGACAGCATGAGCCAGG 379		RIKEN Integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Db	305 GGAGAATGCTTGGATGAGAACTTAAAGATGAACTTGGACAGCATGAGCCAGG 364		Kondo,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
QY	380 TTTCAGAAAGCAGGGAGAACGGGAGCAGCCATATAGACACTCTGGGACA 439		Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-299 (2001)
Db	425 CGCTGAAGACGCAATGCTACTGGTAACTCTGAGCCAGGCGCGAG 484		Please visit our web site ( <a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a> ) for further details.
QY	365 TTCCCCAGAAAGACAGGAGAACGGAGACGAGCCAGGTCACTGACACTCGGGATA 424		e mouse tissues.
Db	440 CCTCTGGAAGAACGCAATGCTACCTGGACTCCPACAGACGCTTAACAAAGCA-GAG 498	FEATURES	Location/Qualifiers
QY	421 CCGCTGAAGACGCAATGCTACTGGTAACTCTGAGCCAGGCGCGAG 484	source	1. . 528
Db	499 ATGGCTGTGTCACCTGAAACAGATGAGTCTCCGGAGGAGGGAGGATGAGAC 518		/organism="Mus musculus"
Db	485 ATGGCTGTGTCACACTGAAACAGATGAGTCTAGAGAGAGCAGGATGAGAC 514		/db_xref="taxon:10090"
QY	559 AACACAGCTGGAGGAGGCCACCGACTCAAGTCGCAATGAAACCATGGCAATT 618		/clone="G830012P05"
Db	545 AACACAGCACAGAGGAGGCCCGCCGGCTCAGGAGCAAGTGAAGACATGGAGCAGATT 604		/clone.lib=RIKEN full-length enriched, mammary gland RCB-0526 JYg-MC(A) cDNA
QY	619 GAGCCTCTACT-CCAGAGCCAGCTCTGAGGTGGAGGAG-AATGATTCGAGAT-GGT 675		/tissue_type="mammary gland"
Db	605 GAGCCTCTACTCCAGAGGCCAGCCCTGAGGTGGCGAGCATGCCAGCATGGGT 664		/cell_line="RCB-0526 JYg-MC(A)"
QY	676 GTGGGACAGTCAGGGCT - GGAGCAGCTGGCTGCTACTGGCTGCCCTCAAAAGAGT 733		
Db	665 GTGGGACAGTCAGGGCTGAAAGCAGCTGGTGTAGCTGAGTCAGTCAGAGAGC 724	BASE COUNT	Query Match 22 1%; Score 437.2; DB 9; Length 528; Best Local Similarity 93.2%; Pred No. 3.3e-80; Matches 490; Conservative 0; Mismatches 33; Indels 3; Gaps 3;
QY	734 ATGAGAATCTGAGGAAGGACTGGAGGACAGGGACACTGGCTG 778	ORIGIN	QY 1434 TAAGTCAGGCCAGAGTAACAGAAGATAAGACTGAGTCTCTCCAGAGAC 1493
Db	725 AGGAGCATCTACAGAGGCCGGCAGGCTCTCAGGAGAGTGGCTG 769		

		FEATURES	LOCATION/QUALIFIERS
		SOURCE	1. .441
Qy	1494	-GCCCLAAGCTGGATACCTTCATGTCAGTGACCGTGGCAGCAGTGATGTTGCAATTA	/organism="Mus musculus"
Db	62	GCCCCRAGCTGGATACCTTATTTCAGTGACCTGGAGATGACGACTTGCAATTA	/strain="C57BL/6J", /db_xref="taxon:0090", /clone="UI-M-BH3-asx-c-07-0-UI", /dev_stage="27-32 days", /lab_host="DH10B (Life Technologies)"
Qy	1553	GTGGCCCAAGACCTGCCTAACCGGAAGTGTGTTTGAGAGTGTTGCAATTA	/note="vector: pTR3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, NIH_BMAP_M_S3_1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR-amplified cDNA inserts from NIH_BMAP_M_S3_3, NIH_BMAP_M_S2, and NIH_BMAP_M_S3_1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, and NIH_BMAP_M_S3_1 libraries in the form of single-stranded circles. The remaining single stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
Db	122	GTGGCCCAAGACCTGCCTAACCGGAAGTGTGTTTGAGAGTGTTGCAATTA	Qy 1553 GTGGCCCAAGACCTGCCTAACCGGAAGTGTGTTTGAGAGTGTTGCAATTA 1552
Qy	1613	CAAGAGAGATGCCAGAAACACACTCCCTGTCACCGG-CCTGACCCACTGG	Db 1613 CAAGAGAGATGCCAGAAACACACTCCCTGTCACCGG-CCTGACCCACTGG 1671
Db	182	CAAGAGAAATGCCAGAAACACACTCCCTGTCACCGG-CCTGACCCACTGG	Db 182 CAAGAGAAATGCCAGAAACACACTCCCTGTCACCGG-CCTGACCCACTGG 241
Qy	1672	AAGCCACATGACCAGTACTGTCGATCAG-CAGGCGCTACTTCAGTGCAGGTT	Qy 1672 AAGCCACATGACCAGTACTGTCGATCAG-CAGGCGCTACTTCAGTGCAGGTT 1730
Db	242	AAGCCACATAACCACTTACCTTTCGATCACGCCACGCCACTTCAGTCAGGTT	Db 242 AAGCCACATAACCACTTACCTTTCGATCACGCCACGCCACTTCAGTCAGGTT 301
Qy	1731	TGCTATAGCTAACCCASGTGCTGGACTCTTGTGTTTAGACAGGGTCACA	Qy 1731 TGCTATAGCTAACCCASGTGCTGGACTCTTGTGTTTAGACAGGGTCACA 1790
Db	302	TGCTATAGCTAACCCAGGTGCTGTCAGTCTTGTGTCAGCTTCATGACGGTT	Db 302 TGCTATAGCTAACCCAGGTGCTGTCAGTCTTGTGTCAGCTTCATGACGGTT 361
Qy	1791	TGACTCTANGTGGATGGGTTGCGGGAGATCTATGGGGTGGTGTAGGGAA	Qy 1791 TGACTCTANGTGGATGGGTTGCGGGAGATCTATGGGGTGGTGTAGGGAA 1850
Db	362	TGACTCTANGTGGATGGGTTGCGGGAGATCTATGGGGTGGTGTAGGGAA	Db 362 TGACTCTANGTGGATGGGTTGCGGGAGATCTATGGGGTGGTGTAGGGAA 421
Qy	1851	GAACCTCTGCCTGCCTCAGCTTATGCTGAAATTATGGGGTGGTGTAGGGAA	Qy 1851 GAACCTCTGCCTGCCTCAGCTTATGCTGAAATTATGGGGTGGTGTAGGGAA 1910
Db	422	AAACTCTCCCTGCCTCAGCTTATGCTGAAATTATGGGGTGGTGTAGGGAA	Db 422 AAACTCTCCCTGCCTCAGCTTATGCTGAAATTATGGGGTGGTGTAGGGAA 481
Qy	1911	AGTGGGGGAAGTWTCTGTAATAAAGGCACTCTTTC	Qy 1911 AGTGGGGGAAGTWTCTGTAATAAAGGCACTCTTTC 1956
Db	482	AGTGGGGGAAGTWTCTGTAATAAAGGCACTCTTCTC	Db 482 AGTGGGGGAAGTWTCTGTAATAAAGGCACTCTTCTC 527
RESULT	25		
Locus	AW490717/c		
DEFINITION	UI-M-BH3-asx-c-07-0-UI.s1 NIH_BMAP_M_S4 Mus musculus mRNA linear EST 24-FEB-2000		
ACCESSION	AW490717		
VERSION	AW490717.1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
TITLE	Normaliziation and subtraction: two approaches to facilitate gene discovery		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	9704477		
COMMENT	Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: mestr@mail.nih.gov		
	The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized prefrontal cortex library. Preparation: M.B. Soares Lab. Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements Seq primer: M13 Forward POLYA=Yes.		
		BASE COUNT	117
		a	115
		c	94
		g	9
		t	115
		ORIGIN	
		Query Match	21.9%; Score 433; DB 9; Length 441;
		Best Local Similarity	98.9%; Pred. No. 2.5e-79;
		Matches	436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy	1534	AGAGTGATGTTGCAATRGTGGCCACGACCTGGCTAACCGGAAGTGTGTTGGAGAT	Db 441 AGAGTGATGTTGCAATRGTGGCCACGACCTGGCTAACCGGAAGTGTGTTGGAGAT 1593
Qy	1594	GGCTCTCTGGACCAAGCAGTCAGAGATGGCCAGAAACACACTCTGTGTCACIGC	Db 381 GGCTCTCTGGACCAAGCAGTCAGAGATGGCCAGAAACACACTCTGTGTCACIGC 1653
Qy	1654	GGCTGACACACTGGCAAGCCACATGACCACTTACTGTCGAGCAGCAGGCCAT	Db 321 GGCTGACACACTGGCAAGCCACATGACCACTTACTGTCGAGCAGCAGGCCAT 262
Qy	1714	TTCAGTGCAGGGTTCTATAGCTCACCAACAGGTGGCTGGCTGGACTCTTGTGTT	Db 261 TTCCAGTGCAGGGTTCTATAGCTCACCAACAGGTGGCTGGCTGGACTCTTGTGTT 202
Qy	1774	TATAGACACGGTCACATGACTCTGTCGCTGCCACSTTATGCTGAAATTATGGGT	Db 201 TATAGACACGGTCACATGACTCTGTCGCTGCCACSTTATGCTGAAATTATGGGT 142
Qy	1834	TGAGGACCTGGCTGACTCTGTCGCTGCCACSTTATGCTGAAATTATGGGT	Db 141 TGAGGACCTGGCTGACTCTGTCGCTGCCACSTTATGCTGAAATTATGGGT 82
Qy	1894	GAGGTGGCATAGGGAAGGTTGGGAAGTTCTGTTAATAAAGGATCTTC	Db 81 GAGGTGGCATAGGGAAGGTTGGGAAGTTCTGTTAATAAAGGATCTTC 1953

QY	1954	TTCGAAAGAAAAAAAGAAAAA	1974	Query Match Best Local Similarity 99.3%; Score 432.2; DB 9; Length 438;
Db	21	TTCTTAACAAACAAACAAA	1	Matches 434; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT	26			SOURCE
BB830459	BB830459	RIKEN full-length enriched, mammary gland sequence.	438 bp mRNA linear EST 19-NOV-2001	ORGANISM
DEFINITION	BB830459	RIKEN full-length enriched, mammary gland sequence.	BB830459 RIKEN full-length enriched, mammary gland clone G930012E24 3', mRNA	Mus musculus
ACCESSION	BB830459		BB830459.1 GI:17008691	
VERSION				
KEYWORDS				
JOURNAL				house mouse.
COMMENT				
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)				
The Institute of Physical and Chemical Research (RIKEN)				
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
Tel: 81-45-503-9222				
Fax: 81-45-503-9216				
Email: genome-res@gsc.riken.go.jp/				
URL: <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a>				
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)				
wagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Otsuka,K., Tanaka,T., Matsuura S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.				
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)				
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.				
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)				
Please visit our web site ( <a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a> ) for further details.				
e mouse tissues.				
FEATURES				
source				
1. .438				
/organism="Mus musculus"				
/db_xref="taxon:10090"				
/clone="G93012E24"				
/clone_id=RIKEN full-length enriched, mammary gland				
RCB-0527 Jig-MC(B) cDNA				
{issue_type="mammary gland"				
/cell_line="RCB-0527 Jig-MC(B)"				
BASE COUNT	102 a	95 c	120 g	121 t
COMMENT				
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)				
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
Tel: 81-45-503-9222				
Fax: 81-45-503-9216				
Email: genome-res@gsc.riken.go.jp/				
URL: <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a>				
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
Normalization and subtraction of cap-trapper-selected cDNAs to				
RESULT	27			
BB795850	BB795850	RIKEN full-length enriched, nullipotent stem cell CRL-2070	519 bp mRNA linear EST 16-NOV-2001	Query Match Best Local Similarity 99.3%; Score 432.2; DB 9; Length 438;
LOCUS	BB795850	BB795850 RIKEN full-length enriched, nullipotent stem cell CRL-2070	Matches 434; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
DEFINITION	BB795850	BB795850 RIKEN full-length enriched, nullipotent stem cell CRL-2070	SOURCE	
ACCESSION	BB795850	BB795850 RIKEN full-length enriched, nullipotent stem cell CRL-2070	ORGANISM	
VERSION	BB795850.1	BB795850.1 GI:16965469	Mus musculus	
KEYWORDS				
JOURNAL				
COMMENT				
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)				
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
Tel: 81-45-503-9222				
Fax: 81-45-503-9216				
Email: genome-res@gsc.riken.go.jp/				
URL: <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a>				
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
Normalization and subtraction of cap-trapper-selected cDNAs to				



	BASE COUNT	166 a	130 c	161 g	90 t
Db	459 GGGGAGACAAATGATCCGCCATTGGACACGCCATTCCGCCAGGGCCGT 400				
Qy	1435 AACGCAAGGCCAGAAGTAAAGAAGTGAAGCTGAGTTCTGCCTCCAG 1494				
Db	399 AGTCCAAGGCCAGAGTAACAGAAAGTGAGATAAGCTGAAATTCTGCTCCAG 340				
Qy	1495 CCCAGCTGATTCCTTATGTCAGTGAAAGCTGAGTTGCAATT 1554				
Db	339 CCCAGCTGACACCTCTATGTCAGTGAAAGCTGAGATAAGCTGAAATTCTGCTCCAG 280				
Qy	1555 GGGCAAGACCTGCTTAACCGGAAGTGTGTTGGAGAGATGGCTCCTGACAGGAGCTCA 1614				
Db	279 GGACCAAGACTCTGCCAACGGGAAGTGTGTTGGAAATGGCTCTGGACAG 222				
Qy	1615 AGAGAGATGCCAGAAAACACACTGCTCCAGTGTCAGTGACCTGAGCTGGAG 1674				
Db	223 -----TTCCCTGTTACTGTGCCCTGACCAACACTGGGAG 187				
Qy	1675 CCAGATGACAGTTACTGTCCGATCAGCAGGGCTACTTCAGTGAGGGTTCT 1734				
Db	186 CCACGTGACAGTTACTGTCTCATGAGCAGGCTACTTCAGTGAGGGTTCT 127				
Qy	1735 TATAGCTACACAGGAGGTGGCTGAGCTCTTGTGTTTATAGAACAGGGTACATGA 1794				
Db	126 TATAGCTACACAGGAGGTGGCTGAGCTCTTGTGTTTATAGAACAGGGTACATGA 67				
Qy	1795 CTCTAAGTGTGAGCTGAGGATCTAGCAGSACTGGGACCTGCTTGAC 1854				
Db	66 CTCTCAGTGGATGGAGACTGAGGACCTATGAGCTGGGA-GACCCCTGCCCTGAC 8				
RESULT	29				
BE031265	BE031265 547 bp mRNA linear EST 09-JUL-2000				
LOCUS	129700 MARC 1PIG Sus scrofa cdna 5', mRNA sequence.				
DEFINITION					
ACCESSION	BB031265.1 GI:8326274				
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiua; Suidae; Sus.				
AUTHORS	Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grossie,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.				
TITLE	Design and use of two pooled tissue normalized cdna libraries for EST discovery in swine				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390				
Email:	smith@email.marc.usda.gov				
Single pass sequencing. Bases called and alt_trimmed with phred and -minmatch 12 options.	Single pass sequencing. Bases called and alt_trimmed with the -minscore 18 options.				
PCR PRIMERS	FORWARD: AGGAAACGCTATGACCAT BACKWARD: GTTTCCAGTCACGAGC Plate: 65 row: H column: 4 Seq primer: ATTAGGAGACTATAG.				
FEATURES	source Location/Qualifiers 1..547 /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC 1PIG" /tissue_type="pooled" /lab_host="DIL10B" (note:"vector: pcMV SPORT6; Site_1: xbaI; Site_2: xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos." )				
RESULT	30				
BB831869	BB831869 450 bp mRNA linear EST 19-NOV-2001				
LOCUS	BB831869 RIKEN full-length enriched, mammary gland RCB-0527				
DEFINITION	JYg-MC(B) CDNA Mus musculus cdna clone G930019H09 3', mRNA sequence.				
ACCESSION	BB831869.1 GI:17101012				
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metacoco; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 450) Akimura,T., Arakawa,T., Caninici,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Koima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakizume,N., Saeki,I.D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sobabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Wataiki,A., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.				
TITLE	Riken Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)				



Query Match 20.6%; Score 407.8; DB 9; Length 453;  
 Best Local Similarity 97.8%; Pred. No. 4e-74; Mismatches 0; Indels 7; Gaps 3;  
 Matches 445; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 1502 TGGATACCTTCTATGTCAGTGACGGGACCGAGGTGATGTTGCAATTGGCCAA 1561  
 1 TGGATACCTTCTATGTCAGTGACGGGACCGAGGTGATGTTGCAATTGGCCAA 59

QY 1552 GACTCTGGTAACGGGAGTGTITGGAGAANGGCCTCTGGACCGTCAAAGAGA 1621  
 1 GACTCTGGTAACGGGAGTGTITGGAGAANGGCCTCTGGACCGTCAAAGAGA 118

Db 60 GACCTGGTAACCGGAAGTGTITGGAGAANGGCCTCTGGACCGTCAAAGAGA 118

QY 1622 TGCCTCAGAACACACTCTGTTACTGCCCTGCACACAGGGAAAGCCATG 1681  
 1 TGCCTCAGAACACACTCTGTTACTGCCCTGCACACAGGGAAAGCCATG 59

Db 119 TGCCTCAGAACACACTCTGTTACTGCCCTGCACACAGGGAAAGCCATG 177

QY 1682 ACCAGTTCAGTGTCCGATCACAGGGGCTACTTCAGTTGAGGGTTTGCTTATAGCT 1741  
 1 ACCAGTTCAGTGTCCGATCACAGGGGCTACTTCAGTTGAGGGTTTGCTTATAGCT 237

Db 178 ACCAGTTCAGTGTCCGATCACAGGGGCTACTTCAGTTGAGGGTTTGCTTATAGCT 237

QY 1742 ACCACCAAGTGCTGACTCTTGTGTTATAGACAGAGGTGCTCCTCTGACAGTCC 1801  
 1 ACCACCAAGTGCTGACTCTTGTGTTATAGACAGAGGTGCTCCTCTGACAGTCC 1801

Db 238 ACCACCAAGTGCTGACTCTTGTGTTATAGACAGAGGTGCTCCTCTGACAGTCC 297

QY 1802 TGGATGGGAGTGTGGAGATCTATGAGCTGGAGCCCTGGCCTGAACTCTCCC 1861  
 1 TGGATGGGAGTGTGGAGATCTATGAGCTGGAGCCCTGGCCTGAACTCTCCC 1861

Db 298 TGGATGGGAGTGTGGAGATCTATGAGCTGGAGCCCTGGCCTGAACTCTCCC 357

QY 1862 TGCCTCCAGCTTATGCTTGAATAATGGGTTAGGTGTTGATAGACAGGGTCACTGCTCAG 1921  
 1 TGCCTCCAGCTTATGCTTGAATAATGGGTTAGGTGTTGATAGACAGGGTCACTGCTCAG 417

Db 358 TGCCTCCAGCTTATGCTTGAATAATGGGTTAGGTGTTGATAGGGAAAGGTGGGAA 417

RESULT 32

BBB35693 BB835693 412 bp mRNA linear EST 19-NOV-2001  
 DEFINITION BBB35693 RIKEN full-length enriched, mammary gland RCB-0527 mRNA  
 ACCESSION BB835693  
 VERSION BB835693.1  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Mus musculus

BBB35693 RIKEN full-length enriched, mammary gland RCB-0527 JyG-MC(B) cDNA sequence.

REFERENCE 1 (bases 1 to 412)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kohama,Y., Konno,H., Kouda,M., Matsunaga,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakizume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,T., Takuji,Akbara,S., Tomaru,A., Toya,T., Watanuki,A., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT

The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-6222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp/  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

Watanuki,M., Fujinake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

mouse tissues.

FEATURES SOURCE

Location/Qualifiers  
 1..412  
 /organism="Mus musculus"  
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 /clone="G930038609"  
 /clone.lib="RIKEN full-length cDNA RCB-0527 JyG-MC(B)"  
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 /cell\_line="RCB-0527 JyG-MC(B)"

BASE COUNT ORIGIN

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 Best Local Similarity 99.3%; Pred. No. 8.6e-74; Mismatches 0; Indels 0; Gaps 0;  
 Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1546 GCAATTAGTAGGGCCAAACCTGGCTAACCGGAAGTGTGTTGGAGAAGGCGCCTCTGG 1605  
 Db 1 GCAATTAGTAGGGCCAAACCTGGCTAACCGGAAGTGTGTTGGAGAAGGCGCCTCTGG 60

QY 1606 ACCAGTCCAGAGAGATGCCAGAACACACTCTCTGTGTTACTGGCCCTGACAC 1665  
 Db 61 ACCAGTCCAGAGAGATGCCAGAACACACTCTCTGTGTTACTGGCCCTGACAC 120

QY 1666 ACTGGGAAGCCACATGACCGTTACTGTTCCATCACAGGAGCTCTTGTGTTATGAGACAGGG 1725  
 Db 181 GGTTGGCTTACGACTACGAGTTACTGTTCCAGTCAGGGCTACTCTGG 180

QY 1786 TCAGATGCTCTAAGTGGATGGGAGTGTGTTGAGGATCTATCAGGGTGG 1845  
 Db 241 TCAGATGCTCTAAGTGGATGGGAGTGTGTTGAGGATCTATCAGGGTGG 300

QY 1846 CGCTTGAACCTCTGCCTGCCTCCAGCTTATGCTTGAATAATGGGGAGGTTGATA 1905  
 Db 301 CGCTTGAACCTCTGCCTGCCTCCAGCTTATGCTTGAATAATGGGGAGGTTGATA 360

QY 1905 GGGAAAGCTGGGAACTTTCGCTGTAATAAATGGAACTTTCCTTC 1956  
 Db 361 GGGAAAGCTGGGAACTTTCGCTGTAATAAATGGAACTTTCCTTC 411

RESULT 33

BB77900 BB77900 423 bp mRNA linear EST 15-NOV-2001  
 DEFINITION BB77900 RIKEN full-length enriched, Nullipotent stem cell CRL-2070 NE mRNA Mus musculus cDNA clone G430042L20 3', mRNA sequence.

ACCESSION BB77900  
 VERSION BB77900.1  
 KEYWORDS EST.

SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	I (bases 1 to 423)
AUTHORS	Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouada,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasada,D., Sato,K., Shiba,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Nagawa,A., Takahashi,F., Takaku-Arahira,S., Tanaka,T., Tomaru,A., Toya,T., Watabiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.)
JOURNAL	Unpublished (2001)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216 Fax: 81-45-503-9222 Email: genome-reseqsc.riken.go.jp/URI: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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source	1. -423 /organism="Mus musculus" /db_xref="taxon:10090" /clone="G430042L20" /clone_lib="RIKEN full-length enriched, Nullipotent stem cell CRL-2070 NE cDNA" /cell_type="Nullipotent stem cell" /cellline="CRL-2070 NE"
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QY	1534 AGAGTGATGTTCGCAATTACTGGCCAGACCTGGCTAACCGGGAGTGTGTTGGAGAT 1593
Db	1 AGACGATGTTGCAATTAGTGCCGAAGACCTGGCTAACCGGAAGTGTGTT-GAAGT 59
QY	1594 GGCGCTCTGGACCAAGAGAGATGCCAGAAACACACTTCCGTTGACTGC 1653
Db	60 GACTCTCTGGACCAGTCCAAAGAGAGATGCCAGAAACACACTTCCGTTGACTGC 119
QY	1654 GCGCTGACCAACTGGGAGGCACATGACCACTAACGTTACGTTGATCAGCAGGCCAC 1713
Db	120 GCCCNGCACACACTGGGAGGCACATGACCACTAACGTTACGTTGATCAGCAGGCCAC 179
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source	1. -403 /organism="Mus musculus" /strain="C5BL/6N" /db_xref="taxon:10090" /clone=IMAGE:555801" /clone.lib="life Tech mouse embryo 13 5dpc 10666014" /tissue_type="embryo" /dev_stage="13.5dpc embryos" /lab_host="DH10B" /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: BASE COUNT 01190 DT. 13.5dpc embryos. pCMV-SPORT2 vector." /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: ORIGIN
Query Match	20.2%; Score 3998; DB 9; Length 403;
Best Local Similarity	99.5%; Pred. No. 1.8e-72; BASE COUNT 110 a 108 c 88 g 97 t

		Matches	401;	Conservative	0;	Mismatches	2;	Indels	0;	Gabs	0;	;
1560	AGACCTGGCTAACCGGAAAGTTTGGAAAGATGGCTCCCTGGACCAGTCAGAGA	1619										/note="Organ: mammary; Vector: pCMV-SPORT6; Site-1: SalI;
1620	GATGCCAGAAAACACACTTCTGTGTCAC TGCGCCTGCAACCACACTGGAGCCACA	1679										Sire_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
343	GATGCCAGAAAACACACTTCTGTGTCAC TGCGCCTGCAACCACACTGGAGCCACA	284.										Library constructed by Life Technologies. Investigator
403	AGACCTGGCTAACCGGAAAGATGGCTCCCTGGACCAGTCAGAGA	344										providing samples: Jeffrey Green, M.D., NIH
	BASE COUNT	107	a	106	c	87	g	90	t	1	others	ORIGIN
	Query Match	19	7%	Score	388	4;	DB	9;	Length	391;		
	Best Local Similarity	99	.5%	Pred.	No.	4.1e-70;						
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	Db	391	ACCTGGCTAACCGGAAAGATGGCTCCCTGGACCAGTCAGAGA	TAG	284.							332
	QY	1623	GCCGAGAAACACACTTCCGTGTCAGCGGCCACTTCCAGTGAGG	GTCAAGAGAT	1682							1682
	Db	331	GCCGAGAAACACACTTCCGTGTCAGCGGCCACTTCCAGTGAGG	CACATGA	272							272
	QY	1683	CCAGTTACTGTCCGATCAGCGAGGCCACTTCAGTGAGGTTTG	CATACTCTG	1742							1742
	Db	271	CCAGTTACTGTCCGATCAGCGAGGCCACTTCAGTGAGGTTTG	CATACTCTG	212							212
	QY	1743	CAACCGAGTGTGGCTGAGCAGCCTTGTGTCAGTGACTCTAGT	1802								1802
	Db	211	CAACCGAGTGTGGCTGAGCAGCCTTGTGTCAGTGACTCTAGT	152								152
	QY	1803	GGATGGGAGPCTGAGGAGRCCTA TGCAGCAGCCTGGCTGACT	CCTGCTGCTGCT	1862							1862
	Db	151	GGATGGGAGPCTGAGGAGRCCTA TGCAGCAGCCTGGCTGACT	CCCTGCTGCT	92							92
	QY	1863	GCCTCCAGCTATTGCTGAATATGGGGAGGTGGAG 1922									
	Db	91	GCCTCCAGCTATTGCTGAATATGGGGAGGTGGAG	32								
	QY	1923	TTTCCTGTGTAATAAAAGGAGCTTTC	1953								
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	BB837528											
	LOCUS	BB837528										
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	JG-MC(B)	RIKEN full-length enriched, mammary gland										
	AUTHORS	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)										
	REFERENCE	CDNA Library Preparation: Life Technologies, Inc.										
	AUTHORS	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)										
	COMMENT	DNA Sequencing by: Washington University Genome Sequencing Center										
	JOURNAL	Tumor Gene Index										
	VERSION	unpublished (1997)										
	KEYWORDS	Other_ESTs: ur79c12.y1										
	SOURCE	Contact: Robert Strainsburg, Ph.D.										
	ORGANISM	Email: cgrabs r@mail.nih.gov										
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	JOURNAL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.										
	VERSION	1 (bases 1 to 391)										
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	COMMENT	Mus musculus										
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	VERSION	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.										
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Email: genome-resgsc.riken.go.jp  
 URL: http://genome.gsc.riken.go.jp/  
 Carrinci,P., Shibata,Y., Hayashita,N., Sugahara,Y., Shibata,K., Itoh  
 , N. Kono, H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. . 10 (10), 1617-1630 (2000)  
 waki,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
 Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura  
 , S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
 Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISEA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. .  
 10 (11), 1757-1771 (2000)  
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carrinci,P., Sugahara  
 , Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.  
 e mouse tissues.

## FEATURES source

1. .393

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/clone\_line="RIKEN full-length enriched, mammary gland

/tissue\_type="mammary gland"

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88 a 87 C 106 g 192 t

BASE COUNT  
ORIGIN

Query Match 19.5%; Score 385.6; DB 9; Length 393;  
 Best Local Similarity 99.0%; Pred. No. 1.6e-69; Indels 0; Gaps 0;  
 Matches 388; Conservative 0; Mismatches 4; Delins 0;

Qy 1565 CTGGCTAACCGGAAGTGTGTTGGAGATGCCCTCTTGACCAAGTCAGAGAGATGC

Db 1 CTGGCTAACCGGAAGTGTGTTGGAGATGCCCTCTTGACCAAGTCAGAGAGATGC 1624

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Qy 1685 AGTTACTGTGTCGGATCAGCAGGGCTACTTCACAGTGCAGGTTTGCTATAGCTACA 1744

Db 121 AGTTACTGTGTCGGATCAGCAGGGCTACTTCACAGTGCAGGTTTGCTATAGCTACA 180

Qy 1745 ACAGAGTGCTGACTCTTGTGTTATAGACAGGGTACATGACTCTAAGTGG 1804

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Qy 1805 ATGGGACTGCTGAGGATCTATGGAGCTGGAGGACCTGGCTGA 1864

Db 241 ATGGGAGTCTGAGGATCTATGGAGCTGGAGGACCTGGCTGA 300

Qy 1865 CTCCAGCTTATGCTGAAATTAGGGTAGGGTAAAGGTCCTTC 1724

Db 301 CTCCAGCTTATGCTGAAATTAGGGTAGGGTAAAGGTCCTTC 360

Qy 1925 TTCTGTGTAATAAAAGGATCTTC 1956

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RESULT 37

BI341090

LOCUS

DEFINITION

ACCESSION

B1341090

571 bp mRNA linear EST 30-JUL-2001

mRNA sequence.

EST

30-JUL-2001

mRNA

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QY 501 GCTGTGTCACCGTAAAGAACAGATGAGTTCTGGAGCAGGGCGAGATGACCAA 560  
Db 238 GATATGCCAAGGCCCAAGGAAGGATCCCAAGCTCACTGGGTCAGAGCTGTCAGG 297  
QY 483 GCTGTGTCACCTCAAGAAGAGTAGACTTGAGCACGAGATGAGACCAA 542  
QY 561 ACAGCTGGAGGAGGCCACGGACTC 588  
Db 238 AGACCCAGATGAGAACCTGGTGTGTCAGACTGCATGGAAAGTGAAGCTCAG 357  
RESULT 38  
DEFINITION 601460641FL1 NIH\_MGC\_66 Homo sapiens cDNA clone IMAGE:3864082 linear EST 20-OCT-2000  
LOCUS BFO38722 mRNA sequence.  
ACCESSION BFO38722  
VERSION BFO38722.1 GI:10745770  
KEYWORDS EST  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 769)  
AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: BCTD/pmp  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution by: The T.M.A.G.E. Consortium (LLNL)  
found through the T.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
http://image.llnl.gov  
plate: LLNL9605 row: a column: 11  
High quality sequence stop: 632.  
Location/Qualifiers  
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Average insert size 1.8 kb. Library constructed by Life  
Technologies."  
BASE COUNT 184 a 212 c 217 g 156 t  
ORIGIN  
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Best Local Similarity 79.0%; Pred. No. 7.4e-66;  
Matches 463; Conservative 0; Mismatches 119; Indels 4; Gaps 2;  
QY 940 AACCTTGAGCTGCCT-GCGACCAATGAGACGGTCAQCCGCGTGGTTTAGAGGCC 998  
Db 1 AACCTTGAGCTGCACCACTGGCAGCTGAGACGCTGAGCCCTGGTTAGAGGCC 60  
QY 999 AGCCCTGAGGATGAGACCCGAGGCTTACACGCCACCCCTGGTATGATGCA 1058  
Db 61 AGCCCTGAGGATGAGACCCGAGGCTTACACGCCACCCCTGGTATGATGCA 117  
QY 1059 TCTCAGATACACCTTGAGCTAAATACCCCTCACCCAGACCTTGCTCCCGCATG 1118  
Db 118 TCTCATGCTTACCTTGAGTGATACCTCCCAGCCGCCCTCAGCTCCAGCATGG 177  
QY 1119 CCTCCCCAAGAAGCTGTGCTGGAGAGGGACGCCTCCAGATGAGAATGTCTCAAGAA 1178  
Db 178 TTACTACGAAACATTTGGCTAGAGAAGCTCACACTCCCCAATCAGGATGTCCTCCAAAGAA 237  
QY 1179 GGTGACAAGTCTCCAAGCCGAGTCCCACTCACTGGTGGCCAGCTCTAGGGAAAGTGTAGG 1238

QY 1299 TCGAAACAGCCAACAGGACACAGAGAAATCCGAAGCAGACAGATGTAAGAA 1358  
Db 358 CCAGAACGCCAACAGGCCAGGTCAAGCTCTGAGCTCTGAGCAAGTGTGAAG 417  
QY 1359 AGGCTTGTGGCTTGGAGAGAACAAATTATCATCAGCCTAGGGACACAACTTAT 1418  
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DEFINITION AL529568 prime, mRNA sequence.  
ACCESSION AL529568  
VERSION AL529568.1 GI:12793061  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 932)  
AUTHORS Li, W.B., Gruber,C., Jesse,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
COMMENT Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
FEATURES source  
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enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pcMVSPORT 6  
vector. Library was normalized. Library was constructed  
by Life Technologies. Contact : Feng Liang Life  
Technologies, a division of Invitrogen 9800 Medical Center  
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610  
8371 Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"  
BASE COUNT 226 a 253 c 242 g 200 t 11 others  
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Query Match 18 0%; Score 354.8; DB 9; Length 932;  
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Db	399	GCTGACAGGAAATCATGAGCTGAAAGAG- <sup>n</sup> CCAACGATGCTGCAGAACCTTGAA 457
Qy	949	CCTGCCCTC-GGGACCATGAGCCGTAGGCCCTGGTTTGAGAGGCCAGCCCTGT 1007
Db	458	CCTGCCACCAGTGGCCAGTCAGACTGTYGACCGCCPGGTTAGAGGCCAGCCCTGT 517
Qy	1008	GGAGATGATGAGCCAGGCTTACAGGCCACCT <sup>n</sup> GGGTAGAGATTGATCTAAC 1067
Db	518	GGA---GGTGTACTGAGCTCCGGCCATCTCCGGTGTAGTATGATCTCAATGC 574
Qy	1068	ACACCTTGAGTAATACCCCTCACCCAGACCTGTGCTCCAGATGCCCTCCCAA 1127
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Qy	1128	GAAGCTGTGCTGGAGGGACGCCTCTCCATGAGAATGCTCCAGAGGTGACAA 1187
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Qy	1188	AGTCCTCCAAGGCCGAGCTCCAGCTC <sup>n</sup> ACTGGTGGCAGCTGAGCTGAGCTAGA 1247
Db	695	AGGCCCAAGGAGGACTCCAGCYCTCACTGGTGGCCAGAGCTGCTCAGGAGCCAGA 754
Qy	1248	TGAGGAGCTGGCTGCTCCCTCTCTCATCGGAATGCTGTCCTGGTCAAGAAC 1307
Db	755	WGAGGAACTGTGTTGG-CYTCCCTATT <sup>n</sup> TGTCGGAATGCCATCTAGGCCAGAAC 813
Qy	1308	GCCCAACAGGACACAGCAGAACATCCGAGCAGCACAGTGTGAAAGATAGGTTGA 1367
Db	814	GCCCCAGAGGCCAGTCAGACTCTCTGTCAGCAAAAGATGTGTAAGGAGCAGCTYGA 873
Qy	1368	TGGCTTGGAGGAGCAGAACAAATTGATCCAGCT 1401
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DEFINITION	u79c12.y1	585 bp mRNA linear EST 25-MAY-2000
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VERSTON	TR:008854	similar to TRAF-INTERACTING PROTEIN ; mRNA
KEYWORDS		sequence.
SOURCE	EST.	
ORGANISM	house mouse.	
COMMENT	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
REFERENCE	1 (bases 1 to 505)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
JOURNAL	Tumor Gene Index	
	Unpublished (1997)	
CONTACT	Robert Strausberg, Ph.D.	
EMAIL	cgapas-r@mail.nih.gov	
TISSUE PROCUREMENT	Jeffrey Green M.D.	
CDNA LIBRARY PREPARATION	Life Technologies, Inc.	
DNA SEQUENCING BY	The T.M.A.G.E. Consortium (LNU)	
CLONE DISTRIBUTION	NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LNU at:	
	image.lnl.gov/image/html/resources.shtml	
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